Resource Summary Report

Generated by dkNET on May 21, 2025

FragGeneScan

RRID:SCR_011929
Type: Tool

Proper Citation

FragGeneScan (RRID:SCR_011929)

Resource Information

URL: https://sourceforge.net/projects/fraggenescan/

Proper Citation: FragGeneScan (RRID:SCR_011929)

Description: A software application for finding fragmented genes in short reads and may be applied to predict prokaryotic genes in incomplete assemblies or complete genomes.

Resource Type: sequence analysis software, software resource, data analysis software, software application, data processing software

Keywords: microbiome, sequence analysis, fragment, gene, short read, bio.tools

Funding:

Availability: Acknowledgement requested, Available for download

Resource Name: FragGeneScan

Resource ID: SCR_011929

Alternate IDs: OMICS_01484, biotools:fraggenescan

Alternate URLs: http://omics.informatics.indiana.edu/FragGeneScan/, https://bio.tools/fraggenescan

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250521T061412+0000

Ratings and Alerts

No rating or validation information has been found for FragGeneScan.

No alerts have been found for FragGeneScan.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 173 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Lustermans JJM, et al. (2025) Extracellular electron transfer genes expressed by candidate flocking bacteria in cable bacteria sediment. mSystems, 10(1), e0125924.

Kifle BA, et al. (2024) Shotgun metagenomic insights into secondary metabolite biosynthetic gene clusters reveal taxonomic and functional profiles of microbiomes in natural farmland soil. Scientific reports, 14(1), 15096.

Oggerin M, et al. (2024) Niche differentiation within bacterial key-taxa in stratified surface waters of the Southern Pacific Gyre. The ISME journal, 18(1).

Rahman MS, et al. (2024) Comprehensive analysis of genomic variation, pan-genome and biosynthetic potential of Corynebacterium glutamicum strains. PloS one, 19(5), e0299588.

Aguilar C, et al. (2024) Actinomycetota bioprospecting from ore-forming environments. Microbial genomics, 10(5).

Wang FQ, et al. (2024) Particle-attached bacteria act as gatekeepers in the decomposition of complex phytoplankton polysaccharides. Microbiome, 12(1), 32.

Rigkos K, et al. (2024) Biomimetic CO2 Capture Unlocked through Enzyme Mining: Discovery of a Highly Thermo- and Alkali-Stable Carbonic Anhydrase. Environmental science & technology, 58(40), 17732.

Miao Y, et al. (2024) DeePhafier: a phage lifestyle classifier using a multilayer self-attention neural network combining protein information. Briefings in bioinformatics, 25(5).

Richy E, et al. (2024) Long-read sequencing sheds light on key bacteria contributing to deadwood decomposition processes. Environmental microbiome, 19(1), 99.

Wongkuna S, et al. (2024) Identification of a microbial sub-community from the feral chicken gut that reduces Salmonella colonization and improves gut health in a gnotobiotic chicken model. Microbiology spectrum, 12(3), e0162123.

Pushkareva E, et al. (2023) Metagenomic Analysis of Antarctic Biocrusts Unveils a Rich Range of Cold-Shock Proteins. Microorganisms, 11(8).

Lücking D, et al. (2023) Extracellular vesicles are the main contributor to the non-viral protected extracellular sequence space. ISME communications, 3(1), 112.

Thapa S, et al. (2023) Exploring the microbial diversity and characterization of cellulase and hemicellulase genes in goat rumen: a metagenomic approach. BMC biotechnology, 23(1), 51.

Zoumplis A, et al. (2023) Impact of meltwater flow intensity on the spatiotemporal heterogeneity of microbial mats in the McMurdo Dry Valleys, Antarctica. ISME communications, 3(1), 3.

Priest T, et al. (2023) Carbohydrates and carbohydrate degradation gene abundance and transcription in Atlantic waters of the Arctic. ISME communications, 3(1), 130.

Kim J, et al. (2023) Comparative analyses of the faecal resistome against ?-lactam and quinolone antibiotics in humans and livestock using metagenomic sequencing. Scientific reports, 13(1), 20993.

Barbosa da Costa N, et al. (2022) A Glyphosate-Based Herbicide Cross-Selects for Antibiotic Resistance Genes in Bacterioplankton Communities. mSystems, 7(2), e0148221.

McCain JSP, et al. (2022) Proteomic traits vary across taxa in a coastal Antarctic phytoplankton bloom. The ISME journal, 16(2), 569.

Zhou F, et al. (2022) PHISDetector: A Tool to Detect Diverse In Silico Phage-host Interaction Signals for Virome Studies. Genomics, proteomics & bioinformatics, 20(3), 508.

Liu CC, et al. (2022) MetaDecoder: a novel method for clustering metagenomic contigs. Microbiome, 10(1), 46.